In the Specification

Please amend the specification as follows. Insertions are indicated by underlining and deletions are indicated by strikeouts and/or double bracketing.

Please amend the paragraphs beginning at page 9, line 29, as follows:

Fig. 6 depicts lysis by CTL 403A/9 of HLA-B*3501 positive EBV-transformed B-cells (HA7-EBV) incubated with the indicated peptides. The peptides tested were: LPAVVGLSPGEQEY (SEQ ID NO:12), PAVVGLSPGEQEY (SEQ ID NO:13) and LPAVVGLSPGEQE (SEQ ID NO:14).

Fig. 7 demonstrates that the fourteen-mer peptide LPAVVGLSPGEQEY (SEQ ID NO:12) is the optimal peptide recognized by CTL 403A/9. The peptides tested were: LPAVVGLSPGEQEY (SEQ ID NO:12), PAVVGLSPGEQEY (SEQ ID NO:13) and AGLPAVVGLSPGEQE (SEQ ID NO:15).

Please amend the paragraph beginning at page 14, line 16, as follows:

Localization of one or more antigenic peptides in a protein sequence can be aided by HLA peptide binding predictions made according to established rules for binding potential (e.g., Parker et al, *J. Immunol.* 152:163, 1994; Rammensee et al., *Immunogenetics* 41:178-228, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health ~~World Wide Web~~ website ~~at URL http://bimas.dcrt.nih.gov~~.

Please amend the paragraph beginning at page 40, line 17, as follows:

A search of 10 amino acid HLA peptide motifs for the HLA-A24 and HLA-Cw4 recognition elements at the National Institutes of Health website ~~(http://bimas.dcrt.nih.gov)~~ indicated that amino acids 16-25 of SEQ ID NO:5 ~~consititute~~ constitute a peptide which may be presented by these HLA molecules. Given the results for HLA-B*3501, the optimal peptides for HLA-A24 and HLA-Cw4 may be a different size or sequence, which can be determined as

described above. This and other alt.M-CSF peptides can be synthesized and tested for HLA binding as described above for HLA-B*3501.